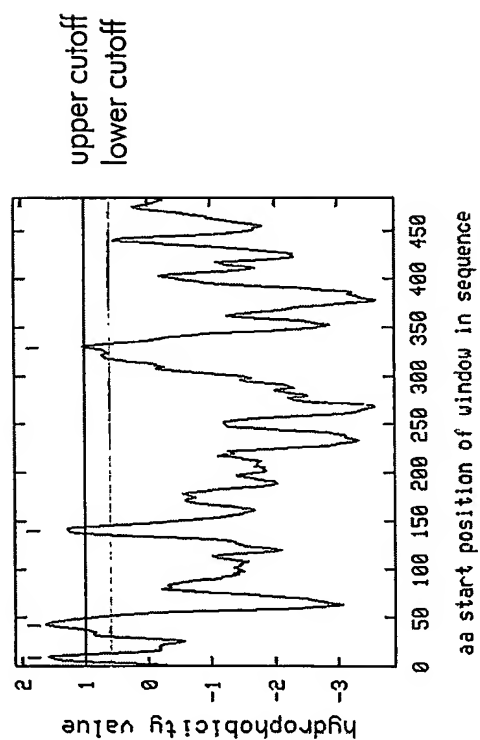
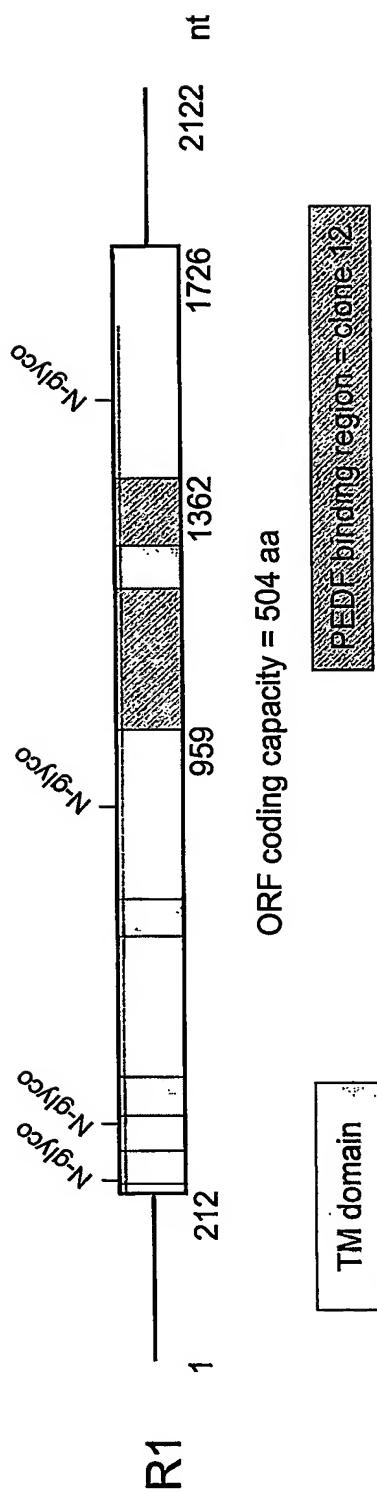
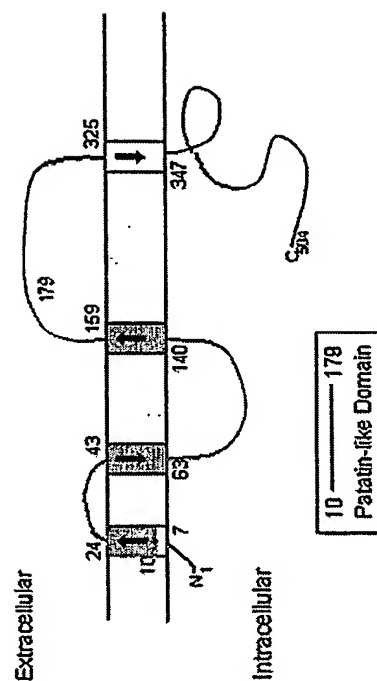


**Figure 1.**

**A.**



o



**BEST AVAILABLE COPY**

Figure 1.  
D.

R1  
adiponutrin

MFPREKTNWISFAGCGFLGVYVGVASCLREHAPFLVANATHIYGASAGALTATATLVTVGCLGEAGAKFIEVSKEARKRFLG  
YDA RG SL F H ATR H LRD RMLF HCVGVLS I P EQTLQVLSDLVRK S NI

PLHPSFNLVKIIRSFLLKVLPA DSHEHASGRLGISLTVSDGENVIISHFN SKDELIQANVCSGFIPIVYCGLI PP SLQGVRYV  
IF S FL QG C C NV QLI KI LV DFR VVD L C F S FR

DGGISDNLPLYELKNTITVSPFSGESDIPCQDSSTNIHEL RVNTTSIQFNLRNLRLSKA LFPPEPLVIREMCKQGYRDGLR  
V V FIDA T P Y Y KVK FLHV DI KL LRLCTG L R FV DLK G I LR L AF

FLQRNGLNRPN-LLALPP-----ARPHGEDKDQAVESAQAE--DYSQLP--GEDH-ILEHLPARLNEALLE  
EEK IC Q G KSSSEGMDPEVAMP SWANMSLDSS SAAL RLEGD LL HLR SILPW ES DT SP AT S

ACVEPTDLLTTLNMLPVRLATAMMVPTLPLESALSFTIRLLEWLDPVPEDIRWMKEQT GSICQ YLVMRAKRKLGRHLPS  
EMKDKGGYMSKIC L I IMSYV L C V LAIVQ VT M D VL LQWV SQVFTRVL CLLEPASRSQM V

RLPEQVELRRVQSLPS-VPLSCAAYREALPGWMNRNLSLGDALAKWEECQRLLLGLFCTNVAFPPEALMRAPADPAPAD  
SSQQA SPCTPE DW CWT C PKGCPAETKAEATPRSI RSS NFFLGKVPAGAEGLS --- SFS EKSL-----

PASPOHQLAGPAPLLSTPAPEARPVIGALGL  
-----

E.

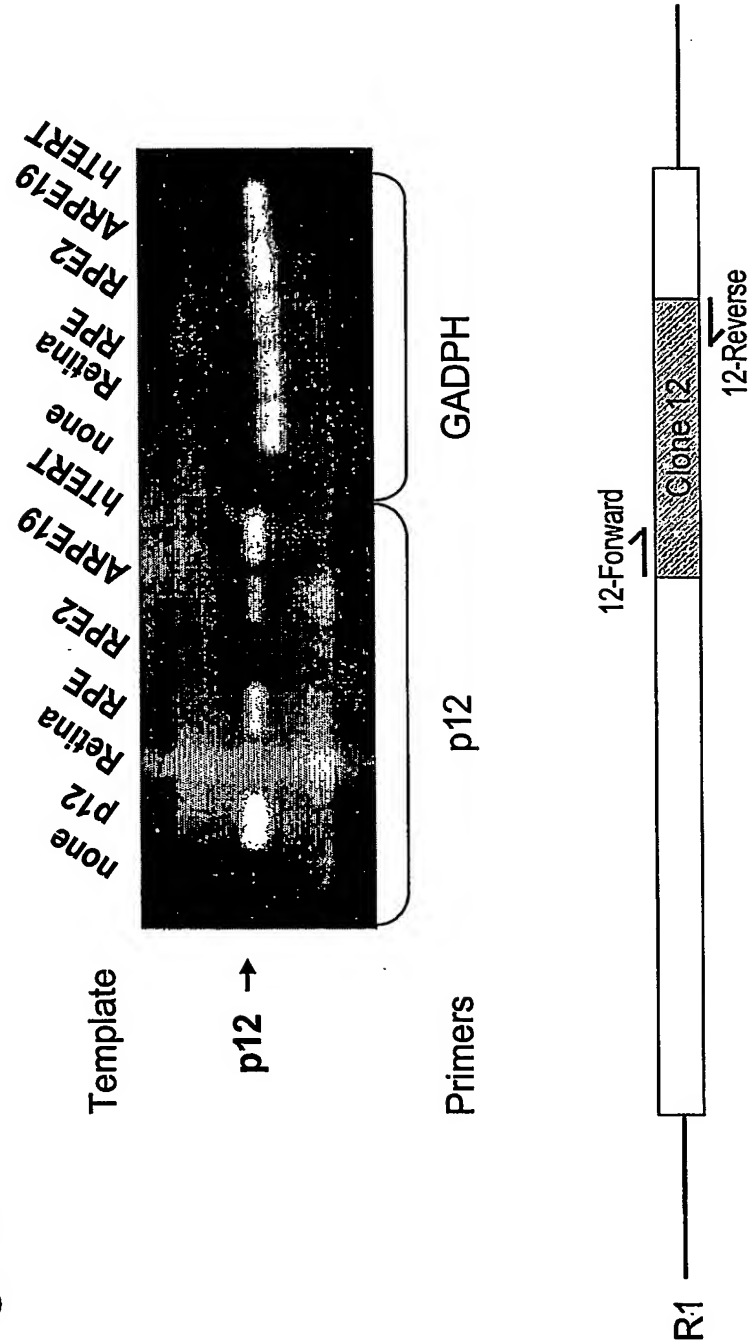
253 GLINRPN PLLALPPARP HGEPKDQAV ESAQAEDYSQ LPGE 293

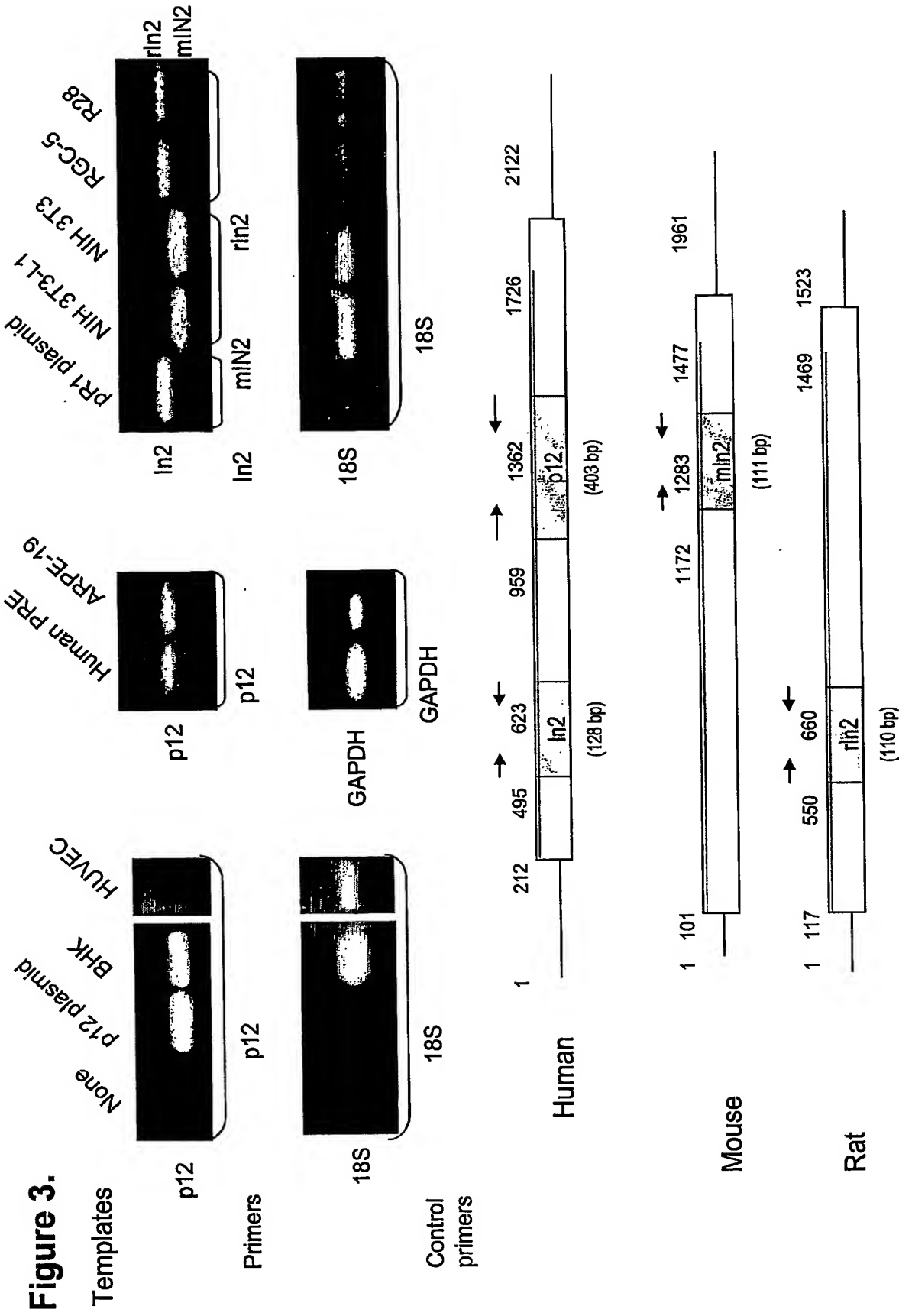
450 T NVAFPPEALR MRAPADPAPA PADPASPOHQ LAGPAPLLST PAPEARPVIG ALGL 504

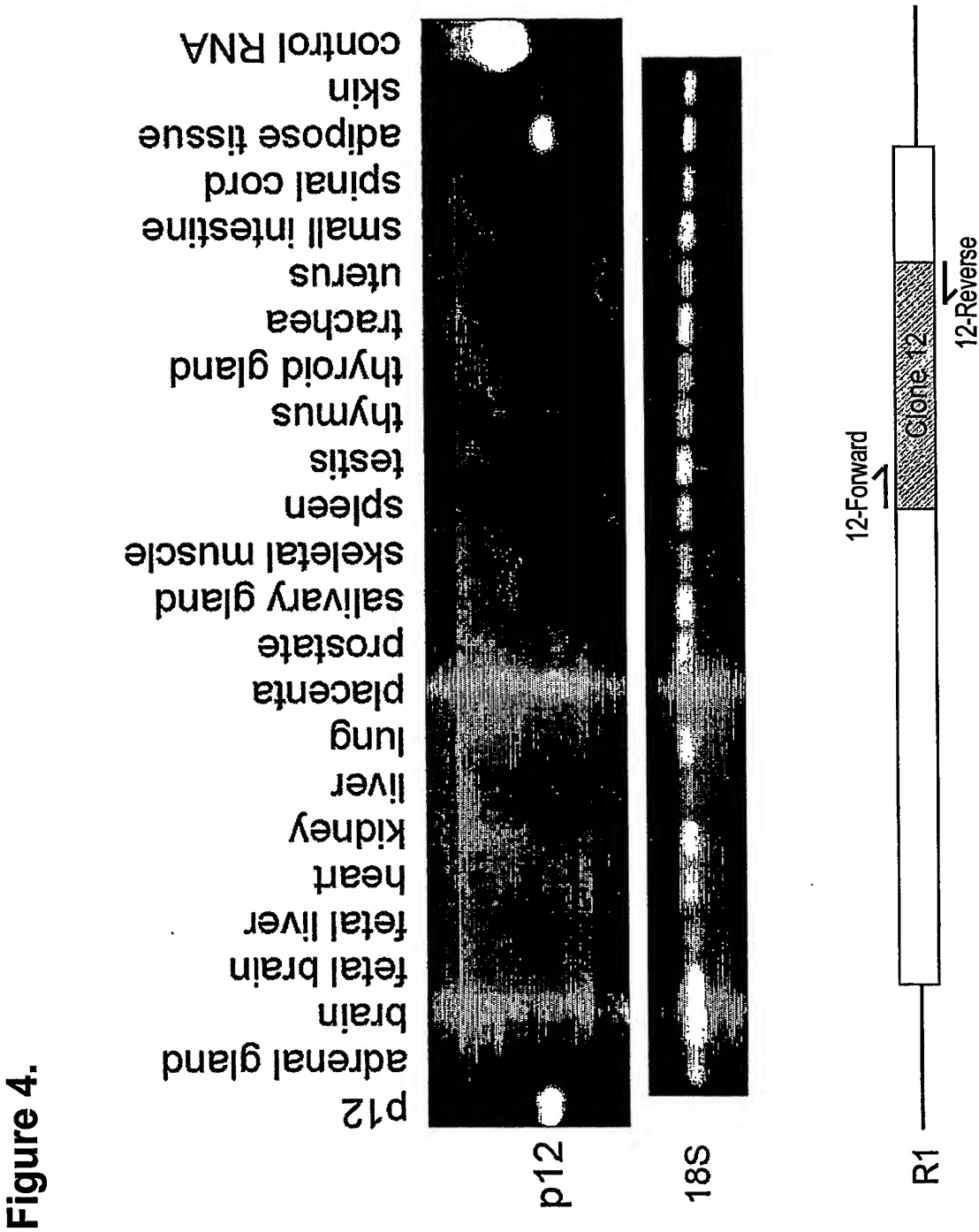
Figure 1.  
F.  
Homologous patatin phospholipase A (PLA) active site in R1: **S**47 and **D**166

Active site serine			
NA	THIYGAS	AGA	LTA R1
YF	DVIGGT	<b>S</b> TGG	LLT Patatin B2
CA	TYVAGL	<b>S</b> GST	WYM cPLA2
Active site aspartic			
SLQ	GVRVVD	GGIS	DNLPYE R1
ARY	EFNLVD	GAVA	TVGDPAL Patatin B2
KSK	KIHVV	<b>D</b> SGL-	TFNLPYP cPLA2

Figure 2.







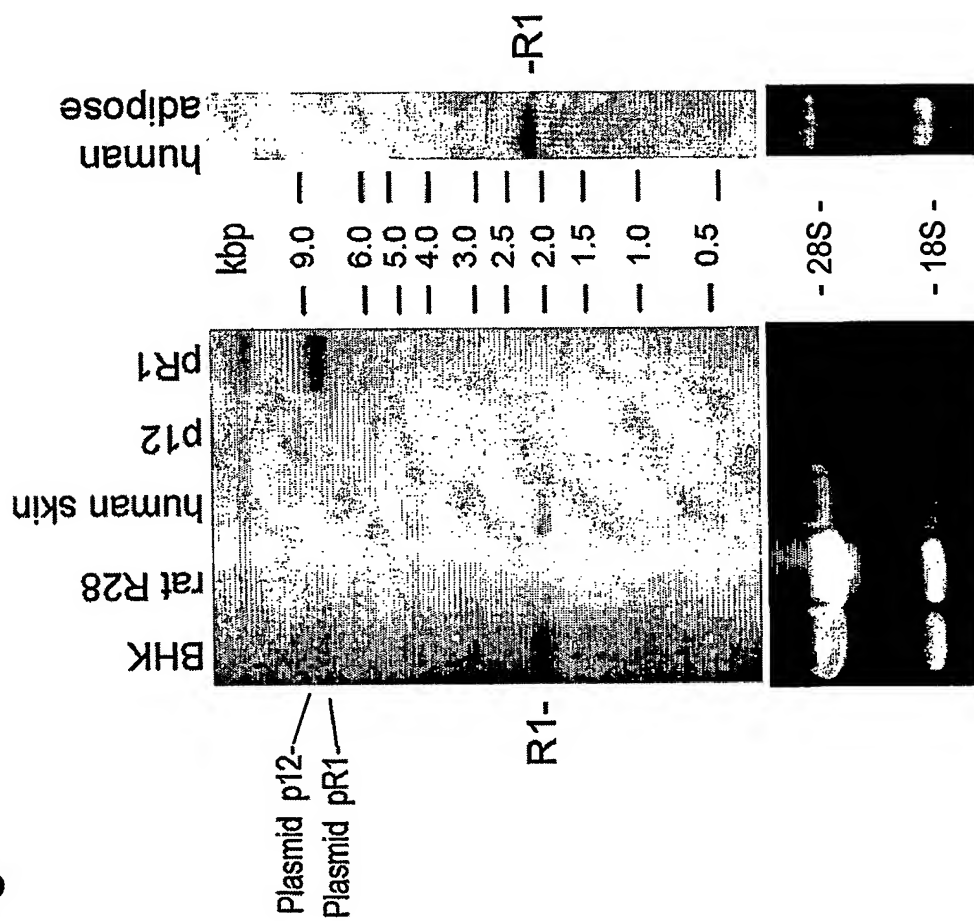


Figure 5.

**Figure 6.**

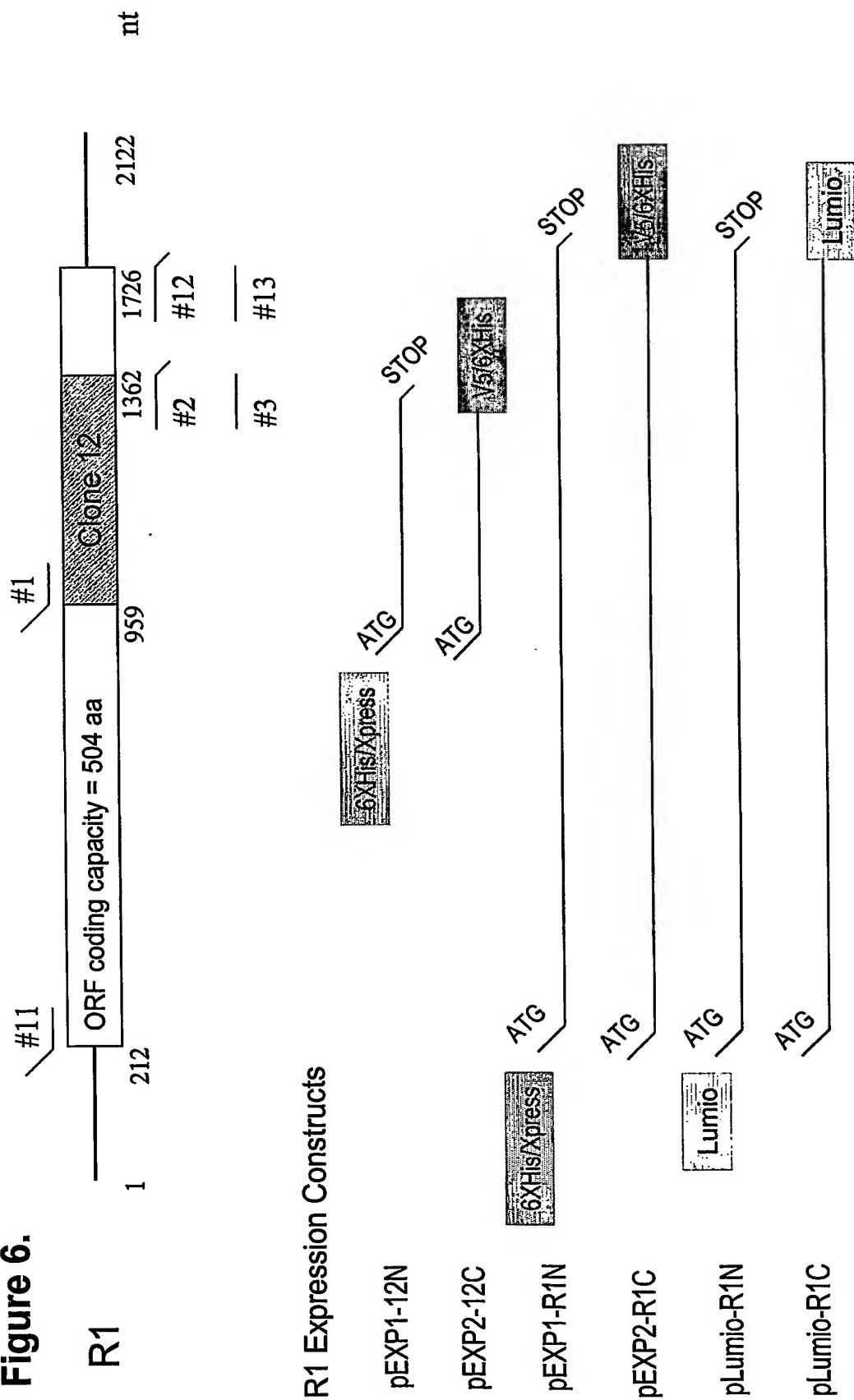
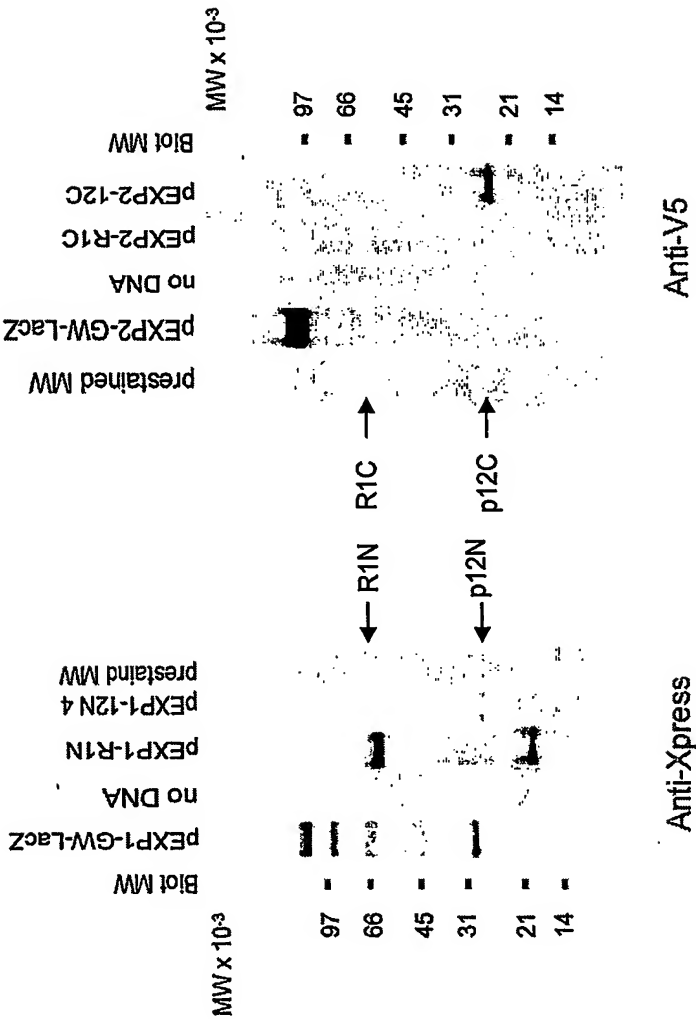


Figure 7.



10/30

Figure 8.

A. p12

Chromatogram

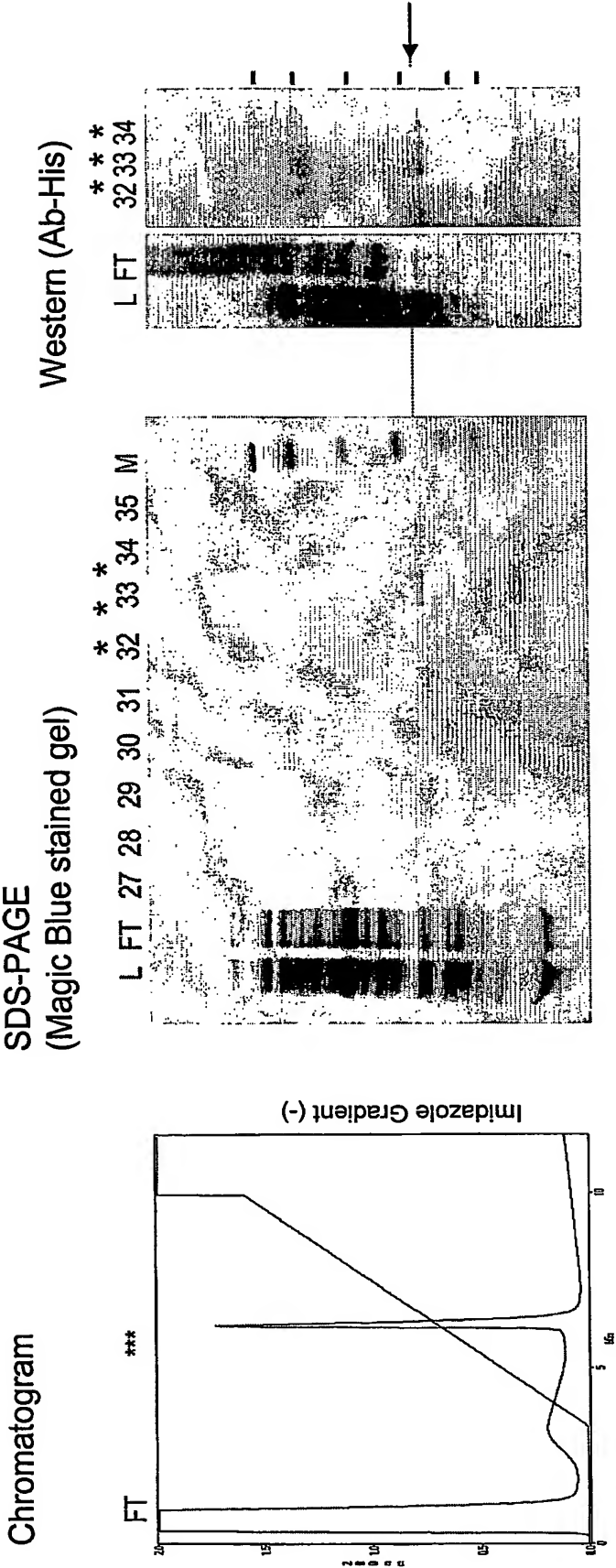
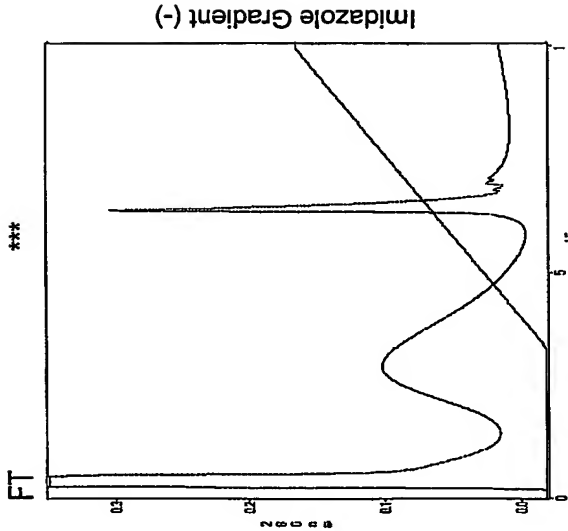


Figure 8.

B. R1

Chromatogram



SDS-PAGE (Coomassie Blue stained gel)

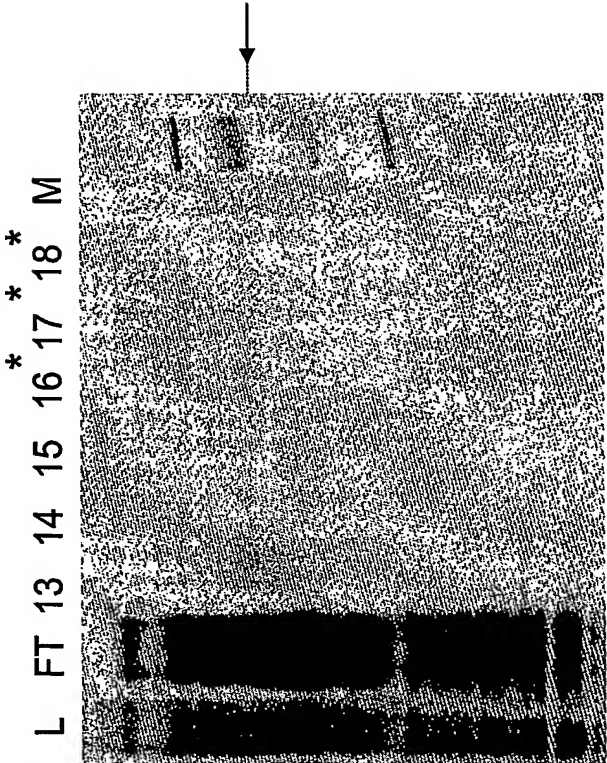


Figure 9.

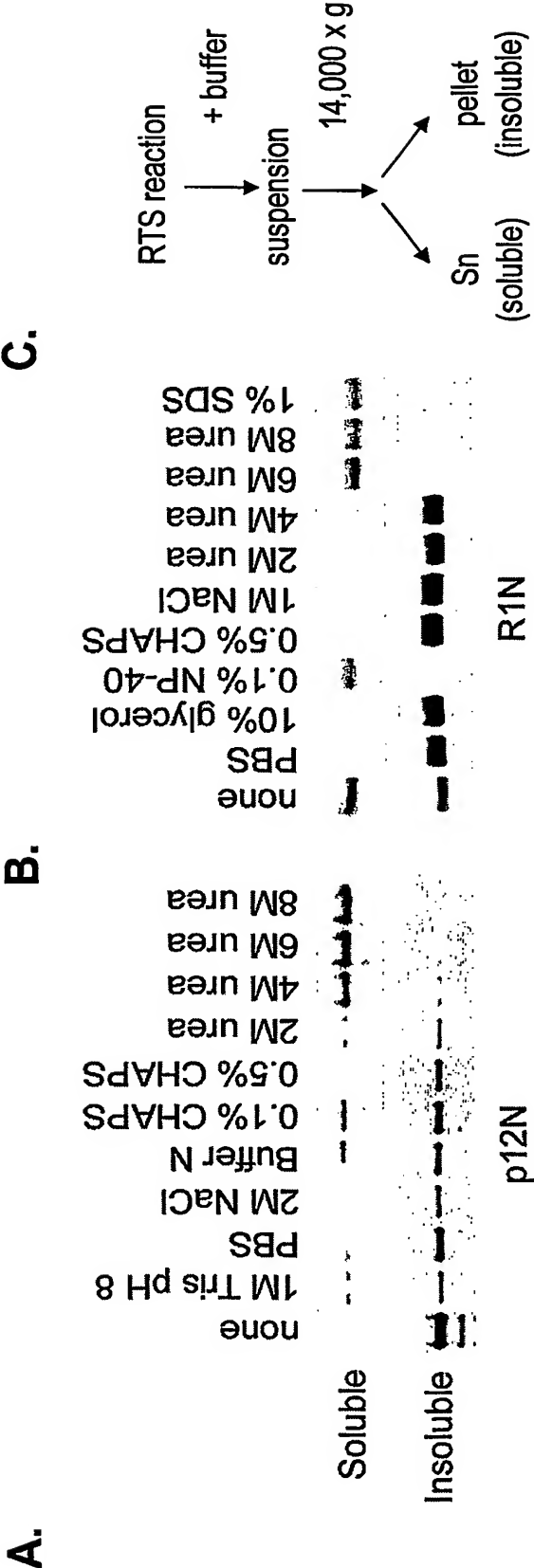
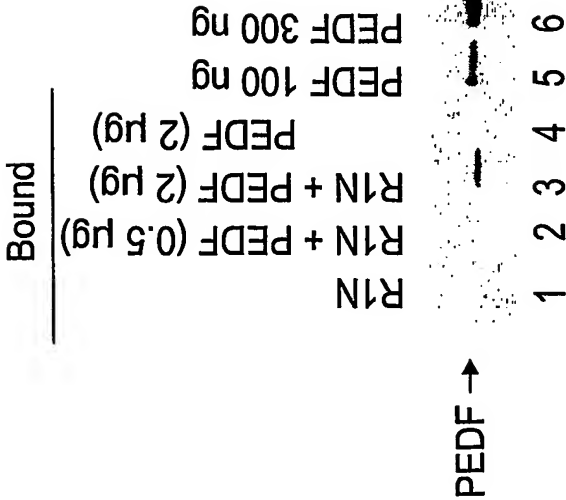


Figure 10.

A. His-tag pull-down



B. complex formation

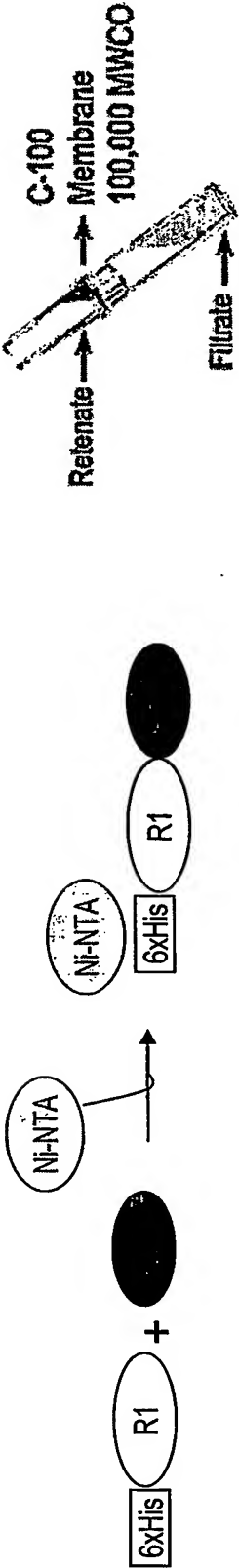
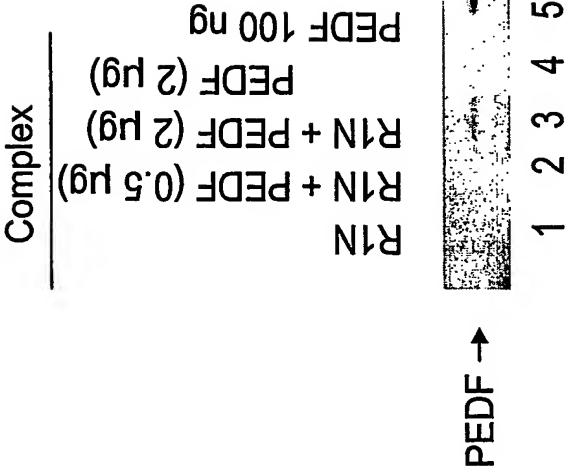
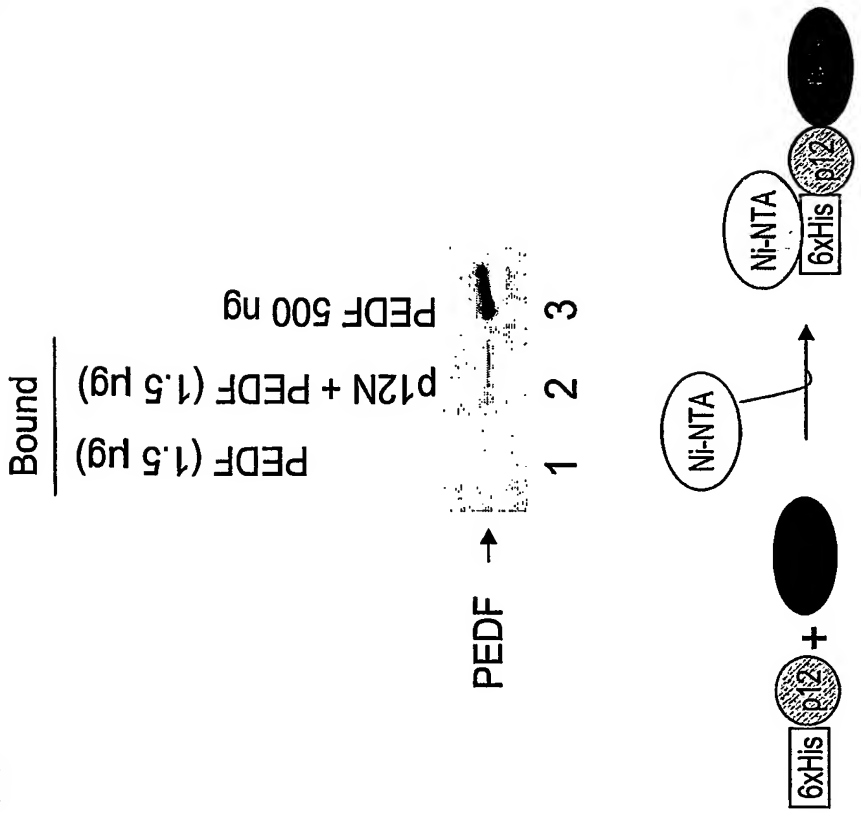


Figure 11.

A.



B.

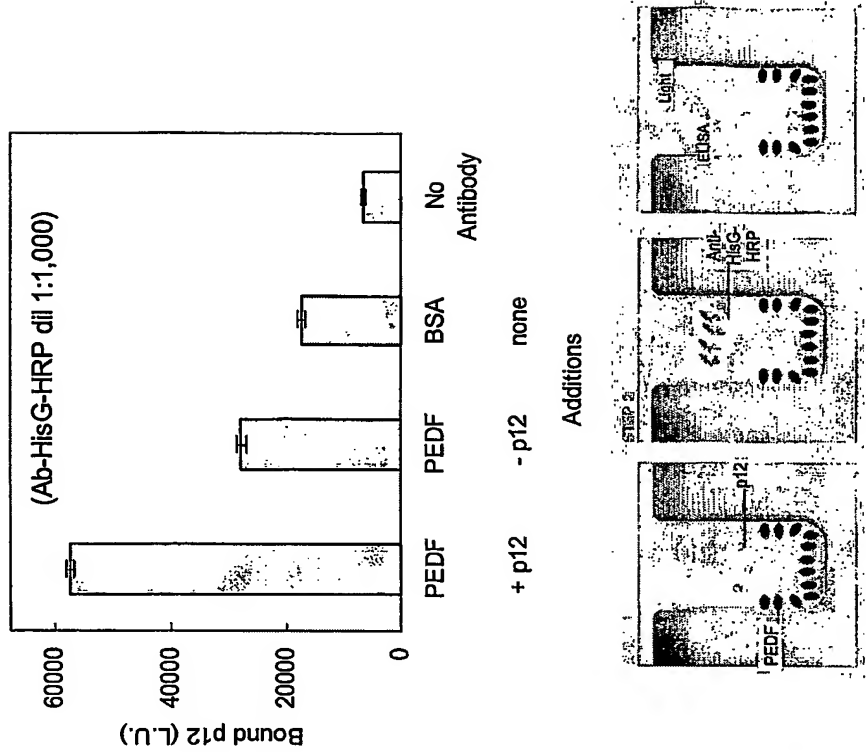


Figure 12.

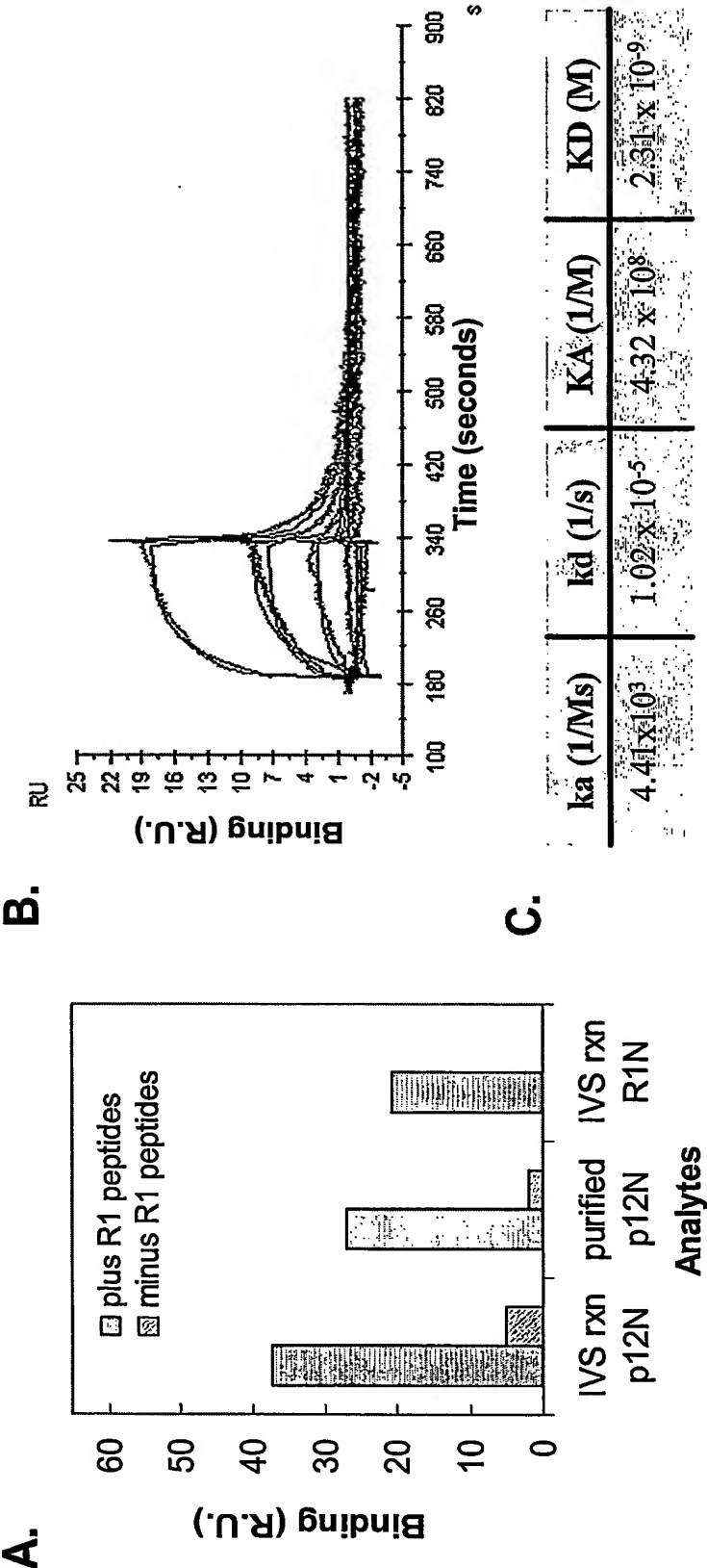


Figure 13.  
A.

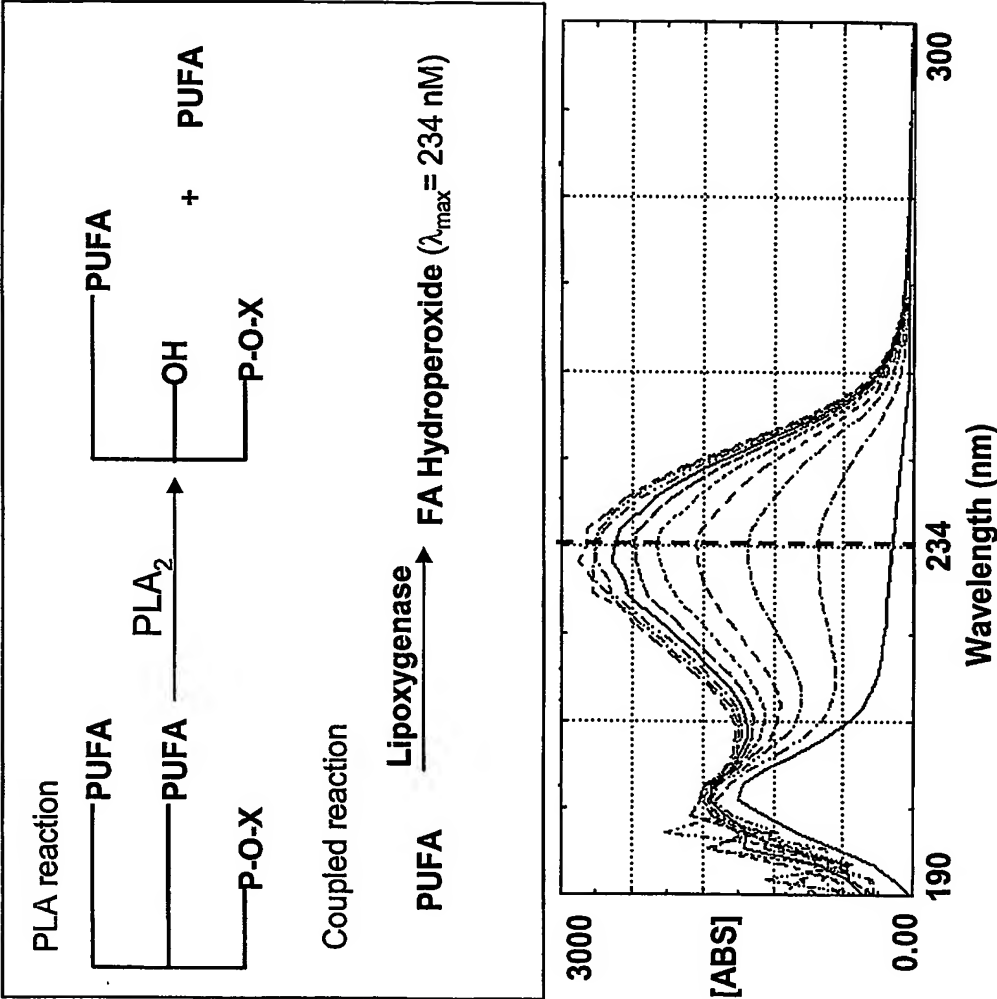
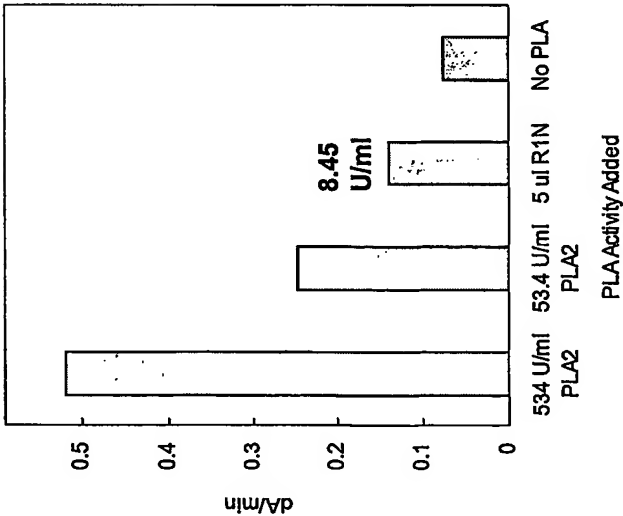
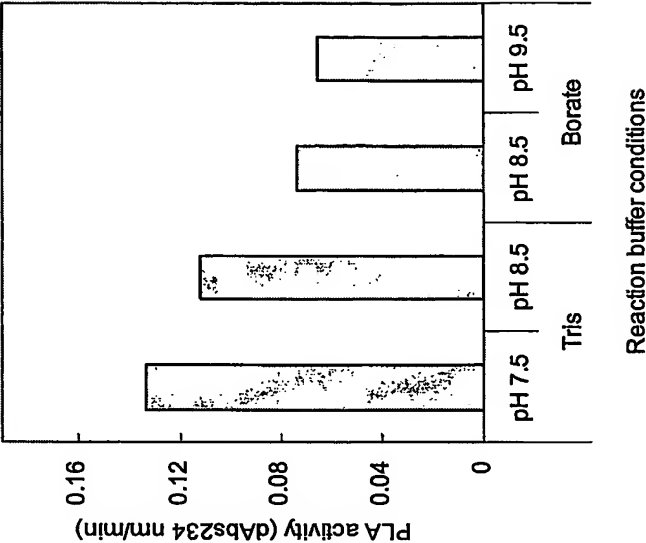


Figure 13.

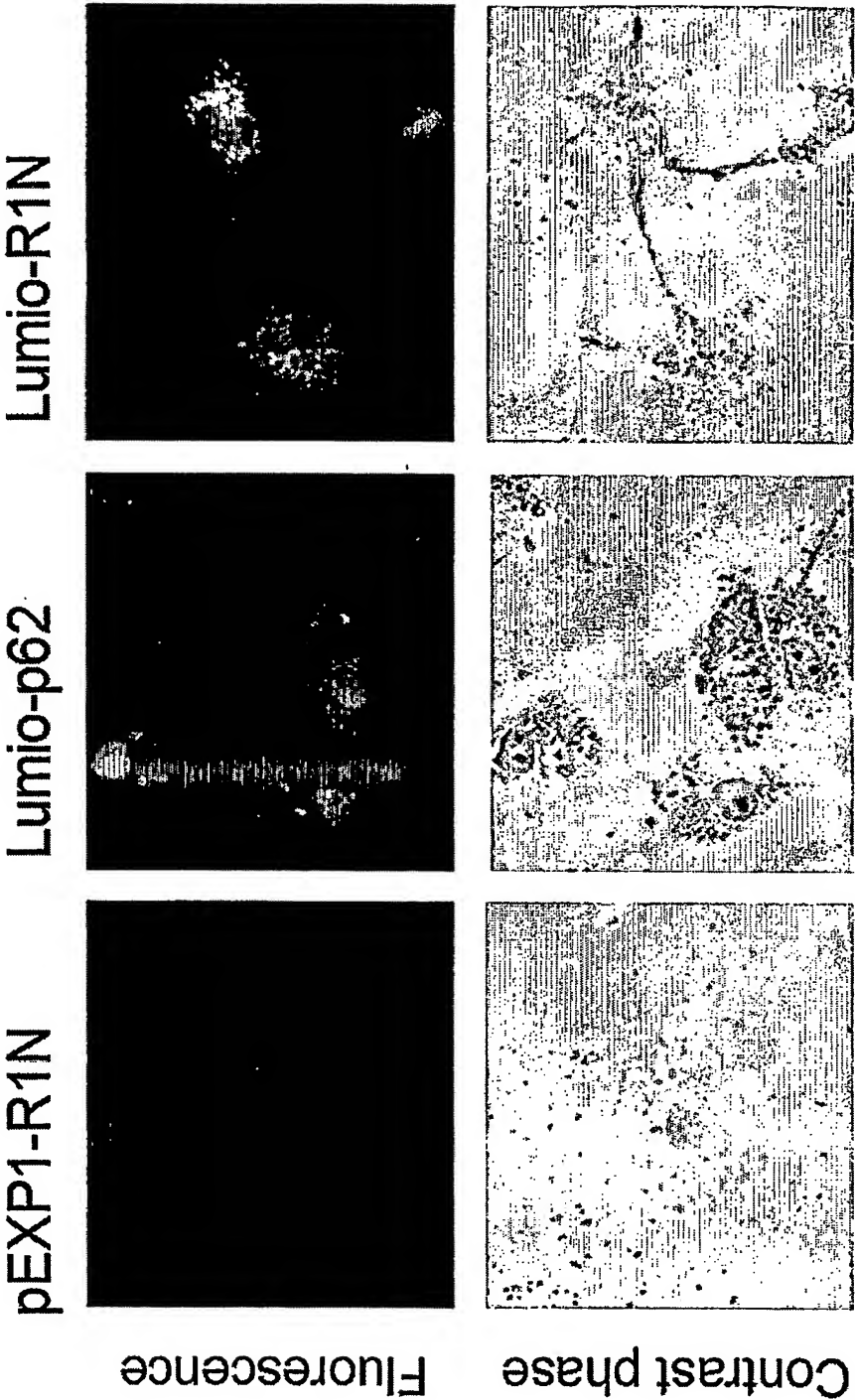
B.



C.



**Figure 14.**  
A. COS-7 cells



**Figure 14.**  
**B. Retinal ganglion RGC-5 cells**

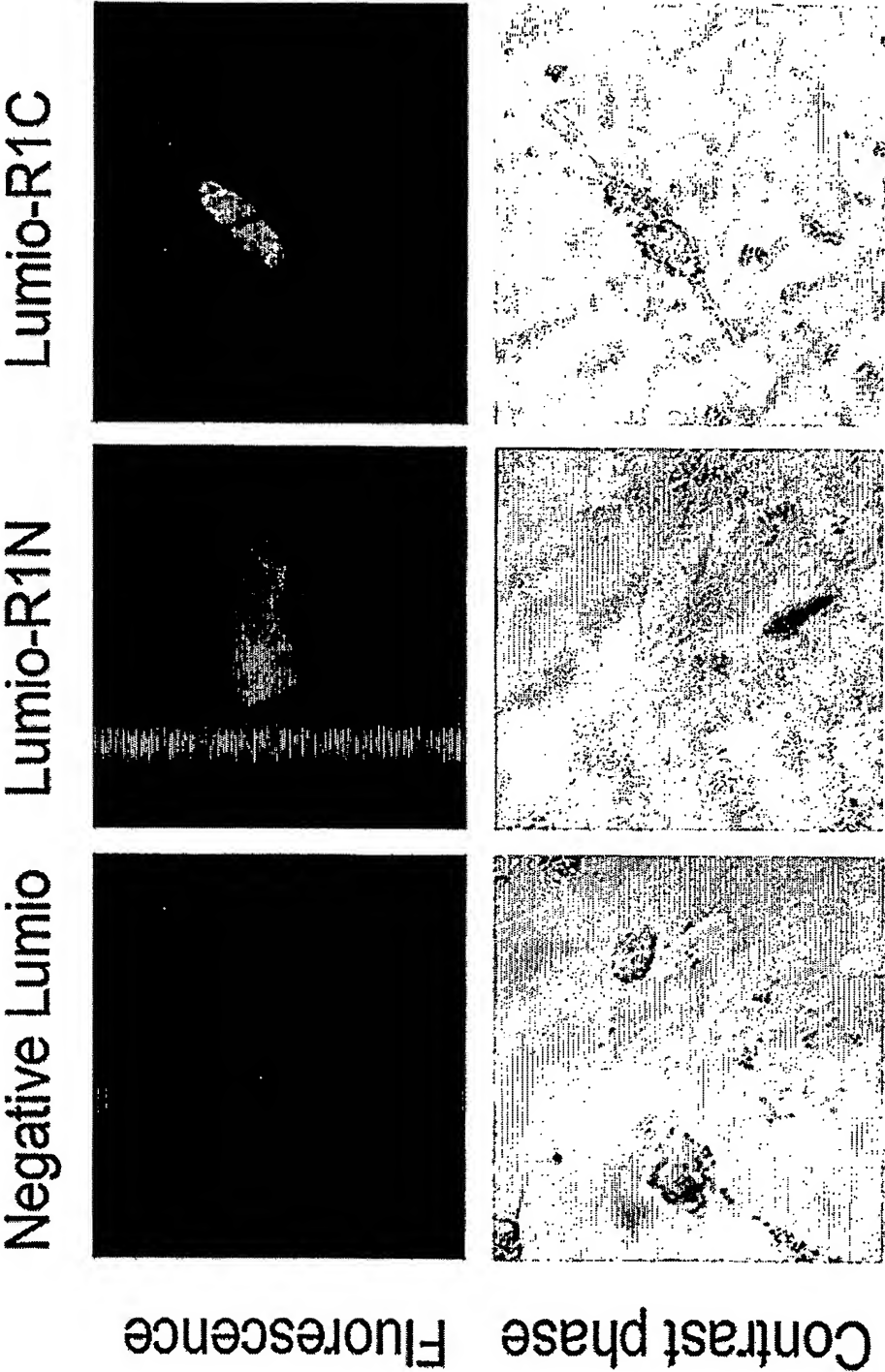


Figure 15.

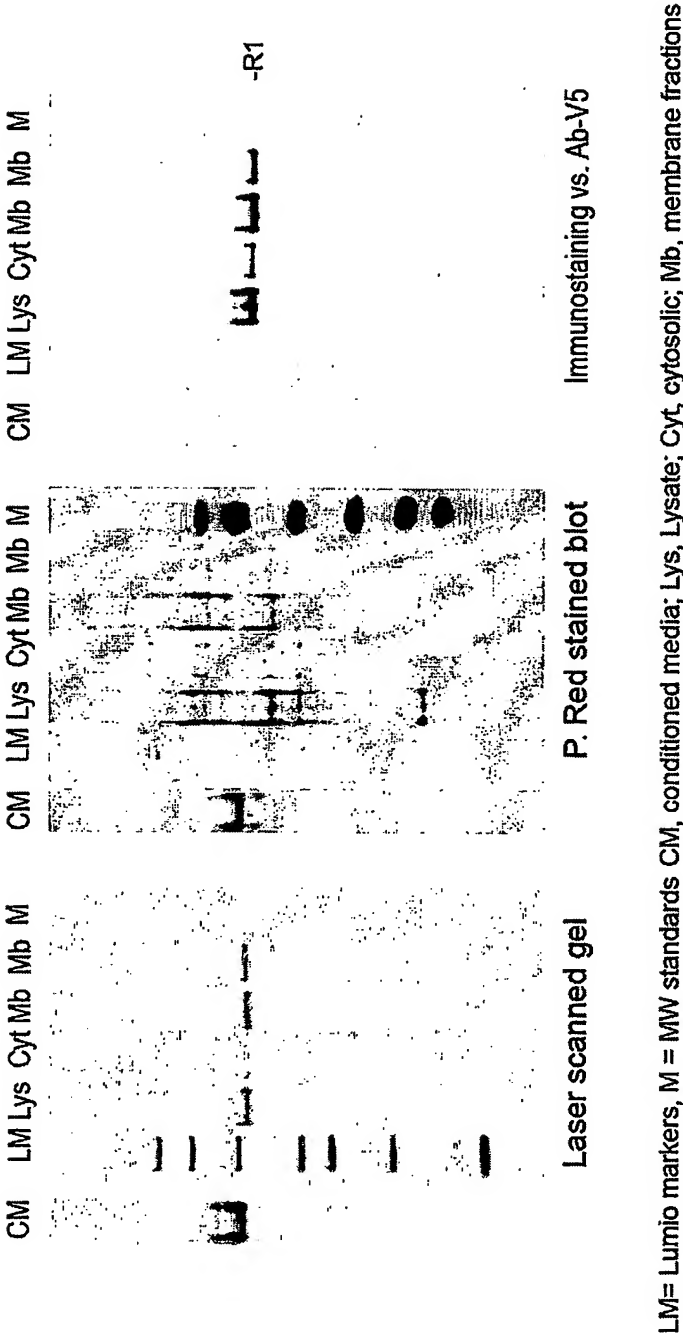




Figure 17.

A.

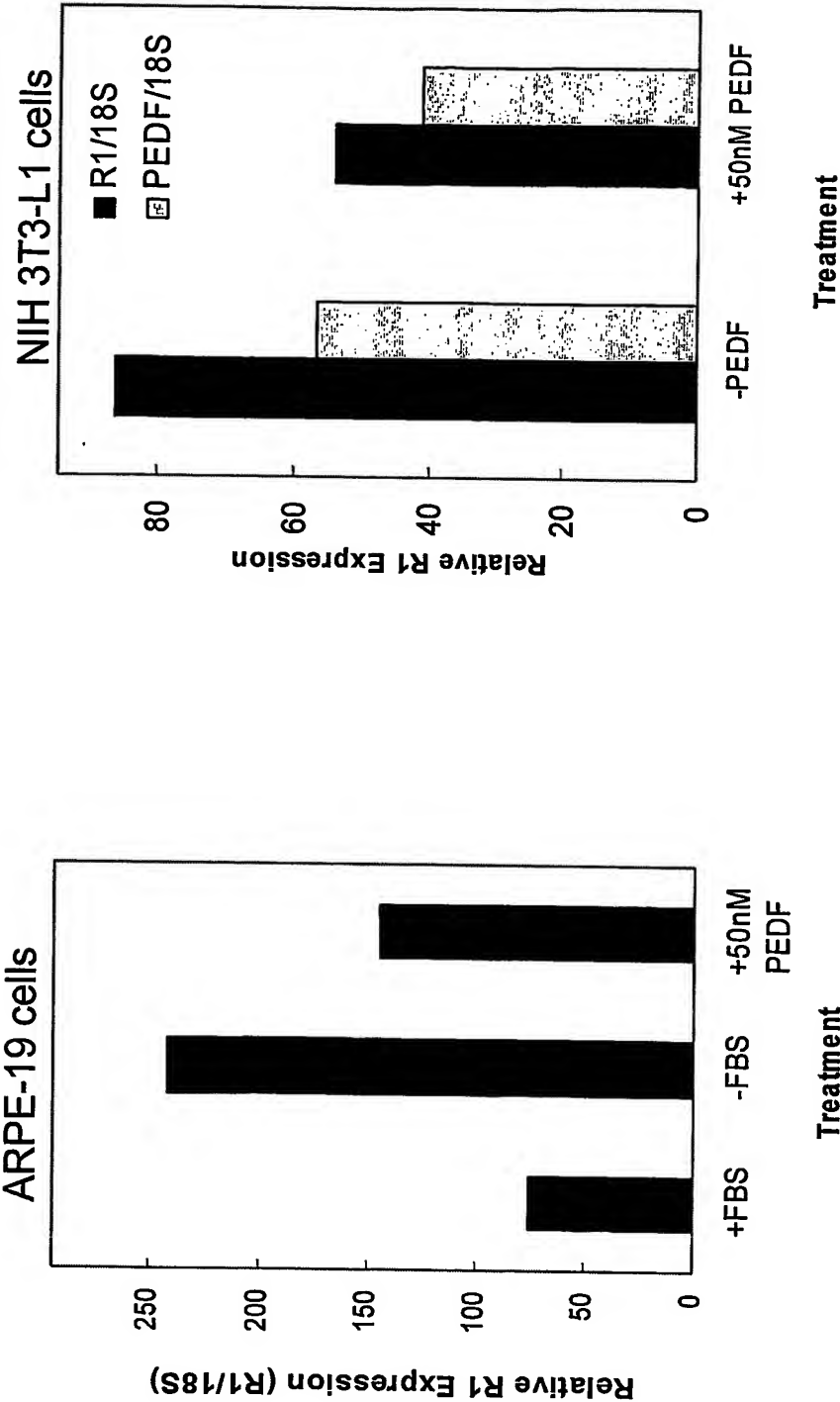


Figure 17.

B.

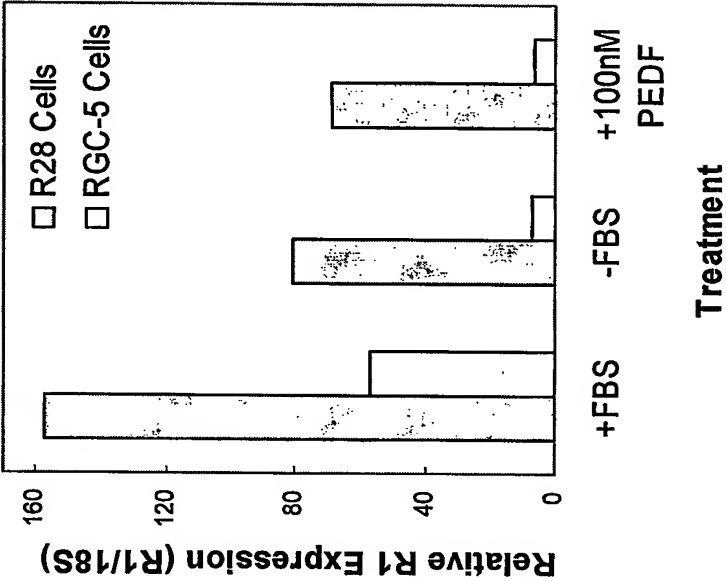


Figure 17.

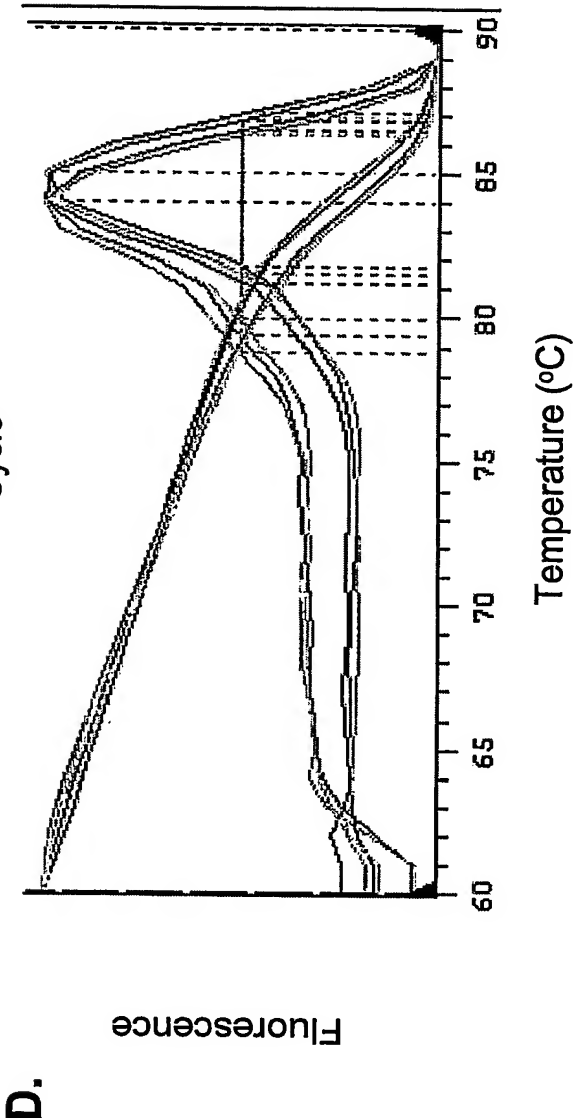
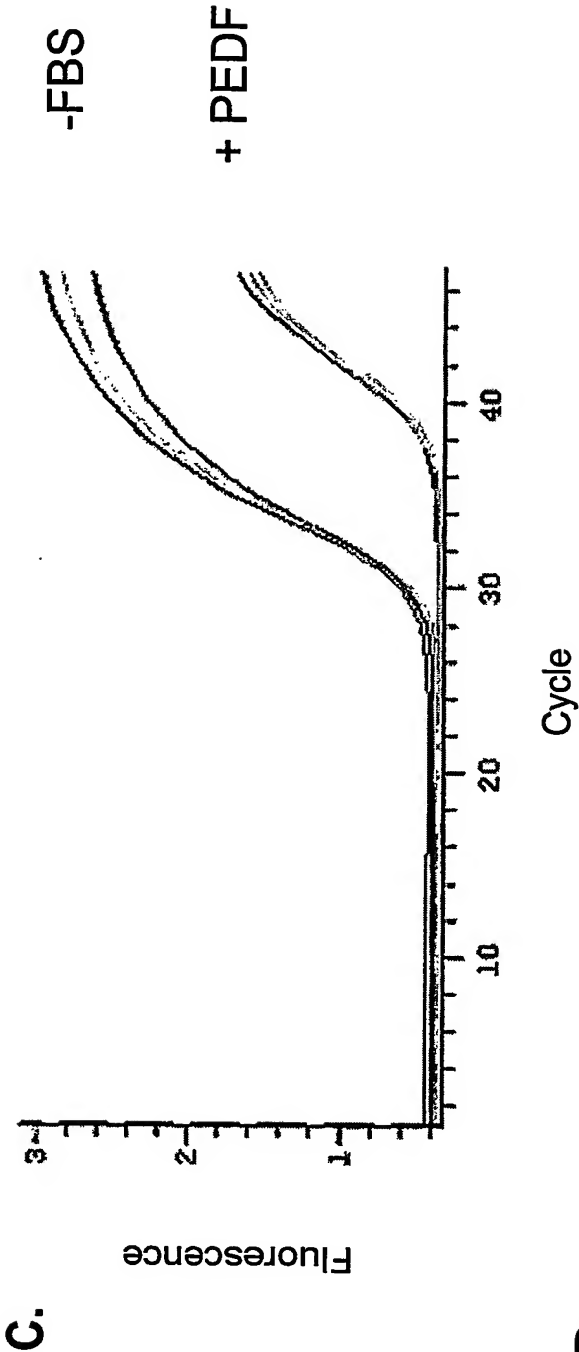
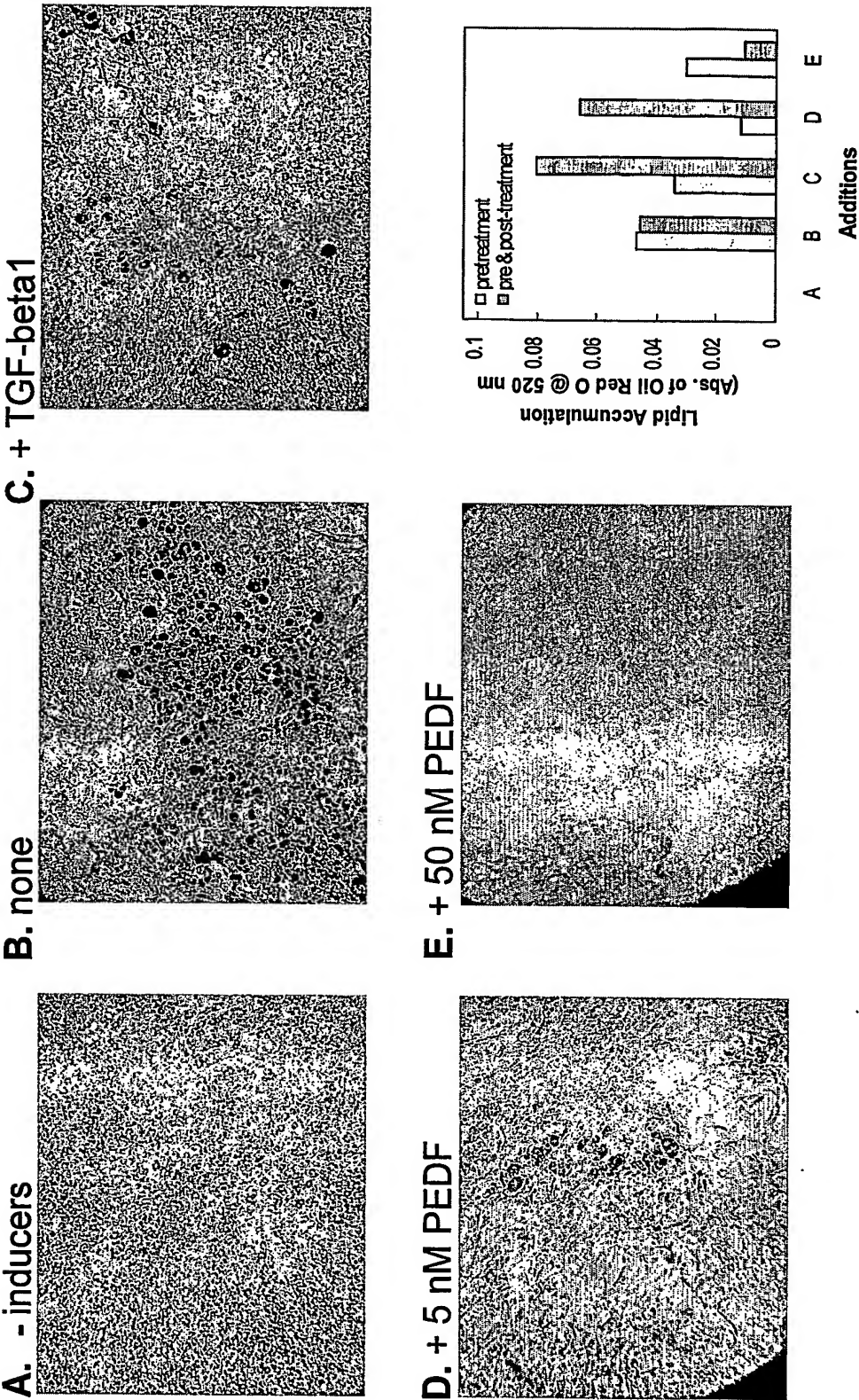


Figure 18.



## Figure 19.

CLUSTAL W (1.82) multiple sequence alignment

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gi|34861242|ref|XP_341961.1|    MFPRETKNWISFAGCGFLGVYHIGVASCLREHAPFLVANATHIYGASAGA 50
gi|16878147|gb|AAH17280.1|      MFPRETKNWISFAGCGFLGVYVGVASCLREHAPFLVANATHIYGASAGA 50
*****.*****.:*****.*****

gi|26327465|dbj|BAC27476.1|      LTATALVTGACLGEAGANIEVSKEARKRFLGPLHPSFNLVKTIRGCLLK 100
gi|34861242|ref|XP_341961.1|    LTATALVTGACLGEAGANIEVSKEARKRFLGPLHPSFNLVKTIRGCLLK 100
gi|16878147|gb|AAH17280.1|      LTATALVTGVCLGEAGAKFIEVSKEARKRFLGPLHPSFNLVKIIRSFLK 100
*****.*****.:*****.***

gi|26327465|dbj|BAC27476.1|      TLPADCHERANGRLGISLTRVSDGENVIISHFSSKDELIQANVCSTFIPV 150
gi|34861242|ref|XP_341961.1|    TLPADCHTRASGRGLISLTRVSDGENVIISHFSSKDELIQANVCSTFIPV 150
gi|16878147|gb|AAH17280.1|      VLPADSHEHASGRGLISLTRVSDGENVIISHFNKDELIQANVCSTFIPV 150
****.*:*.*****.*****

gi|26327465|dbj|BAC27476.1|      YCGLIPPTLQGVRYVDGGISDNLPLYELKNTITVSPFSGESDIPCQDSST 200
gi|34861242|ref|XP_341961.1|    YCGLIPPTLQGVRYVDGGISDNLPLYELKNTITVSPFSGESDIPCQDSST 200
gi|16878147|gb|AAH17280.1|      YCGLIPPSLQGVRYVDGGISDNLPLYELKNTITVSPFSGESDIPCQDSST 200
*****.*****.*****

gi|26327465|dbj|BAC27476.1|      NIHELRTNTSIQFNLRNLRLSKALFPPEPMVLREMCKQGYRDGLRFLR 250
gi|34861242|ref|XP_341961.1|    NIHELRTNTSIQFNLRNLRLSKALFPPEPMVLREMCKQGYRDGLRFLR 250
gi|16878147|gb|AAH17280.1|      NIHELRTNTSIQFNLRNLRLSKALFPPEPLVLRMCKQGYRDGLRFLQ 250
*****.*****.:*****.

gi|26327465|dbj|BAC27476.1|      RNGLLNQPNPLLALPPVVPQEEDAEEAAVVEERAGEEDQLQPYRKDRILE 300
gi|34861242|ref|XP_341961.1|    RNGLLNQPNPLLALPPVVPQEEDAEEAAVTEERTGGED-----RILE 292
gi|16878147|gb|AAH17280.1|      RNGLLNRPNPLLALPPARPHGPEKDKQAVESAQAEDYSQLP--GEDHILE 298
*****.*****.*: : : : * . : : . : ***

gi|26327465|dbj|BAC27476.1|      HLPARLNEALLEACVEPKDLMTTLSNMLPVRLATAMMVPTLPLESAVSF 350
gi|34861242|ref|XP_341961.1|    HLPARLNEALLEACVEPKDLMTTLSNMLPVRLATAMMVPTLPLESAVSF 342
gi|16878147|gb|AAH17280.1|      HLPARLNEALLEACVEPTDLLTTLSNMLPVRLATAMMVPTLPLESALSF 348
*****.*****.*:*****.*****

gi|26327465|dbj|BAC27476.1|      TIRLLEWLPDVPEDIRWMKEQTGSICQYLVMRKRKLGDHLP SRLSEQVE 400
gi|34861242|ref|XP_341961.1|    TIRLLEWLPDVPEDIRWMKEQTGSICQYLVMRKRKLGDHLP SRLSEQVE 392
gi|16878147|gb|AAH17280.1|      TIRLLEWLPDVPEDIRWMKEQTGSICQYLVMRKRKLGRHLP SRLPEQVE 398
*****.*****.*****

gi|26327465|dbj|BAC27476.1|      LRRQSLPSVPLSCATYSEALPNWVRNNLSLGDALAKWEECQRQLLLGLF 450
gi|34861242|ref|XP_341961.1|    LRRQSLPSVPLSCATYSEALPNWVRNNLSLGDALAKWEECQRQLLLGLF 442
gi|16878147|gb|AAH17280.1|      LRRVQSLPSVPLSCAAYREALPGWVRNNLSLGDALAKWEECQRQLLLGLF 448
***.*****.*:*****.*****

gi|26327465|dbj|BAC27476.1|      CTNVAFFPPDALRMRAPAS--PTAADPATPDPPGLPPC----- 486
gi|34861242|ref|XP_341961.1|    CTNVAFFPPDALRMRAPAS--PTATDPATPDPSGLPPC----- 478
gi|16878147|gb|AAH17280.1|      CTNVAFFPEALRMRAPADPAPADPASQHQLAGPAPLLSTPAPEARPV 498
*****.*****.*: : : : * . : : *

gi|26327465|dbj|BAC27476.1|      -----
gi|34861242|ref|XP_341961.1|    -----
gi|16878147|gb|AAH17280.1|      IGALGL 504

```

## Figure 20. (1 of 4)

CLUSTAL W (1.82) multiple sequence alignment

```
gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
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GGCACGAGGGCGGCCCCAGTCAGACGCAGGCAGCCCCAAAGCCTGAACAG 50

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
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GCAGGGCCAGACCCAGCTTCTTCGCCTCCGCCAGCGGGGACCCCGAGCTA 100

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
-----
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GAGCCGCAGCGGGACCTGCCCGGCCCCCGGCTCCAGCGAGCGAGCGGCGA 150

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
-----
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CCGGCGGGGACCCAGGTTATCAA-GACTGCGGGACCCACTGCCCGCAGG 83
GCAGCGCGCTCACAGAGCCTGGCCGCCACGGAACCCGGGGCCCGGCGG 200
      * * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
-----
ACATCGAGTCACGATGTTCCCGAGGGAGACCAAGTGGAACATCTCATTCG 94
ACGTCTAATCACGATGTTCCCAAGGGAGACCAAGTGGAACATCTCGTTTCG 133
CCGCC--GCCGCGATGTTTCCCGCGGAGAACGCTGGAACATCTCGTTTCG 248
      * * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
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CTGGCTGCGGCTTCCCTCGGGGTCTACCACATTGGAGTGGCCTCCTGCCTC 183
CGGGCTGCGGCTTCCCTCGGGGTCTACTACGTCGGCGTGGCCTCCTGCCTC 298
* * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
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CGTGAGCACGCGCCCTTCCCTGGTGGCCAACGCCACTCACATCTACGGAGC 194
CGTGAGCACGCGCCCTTCCCTGGTGGCCAACGCCACTCACATCTACGGAGC 233
CGCGAGCACGCGCCCTTCCCTGGTGGCCAACGCCACGCACATCTACGGCGC 348
** * * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
-----
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CTCGGCAGGGGCGCTTACCGCCACAGCGCTGGTCACTGGGGCCTGCCTGG 283
CTCGGCCGGGGCGCTCACCGCCACGGCGCTGGTCACTGGGGCTGCGCTGG 398
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gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
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GCGAAGCGGGTGCCAACATTATTGAGGTGTCCAAGGAGGCTCGGAAGCGG 333
GTGAGGCTGGTGCCAAGTTCATTGAGGTATCTAAAGAGGCCCGGAAGCGG 448
* * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
-----
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TTCCTGGGCCCCCTGCACCCCTCCTTCAACCTGGTAAAGATCATCCGCAG 498
***** * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
-----
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TTGTCTACTGAAGACCCCTGCCTGCTGATTGCCACACGCGTGCCAGCGGAC 433
TTTCTGCTGAAGTCTTGCCTGCTGATAGCCATGAGCATGCCAGTGGGC 548
      * * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
-----
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GCCTGGGCATCTCCCTGACTCGAGTTTCGGATGGAGAGAAATGTCATCATA 483
GCCTGGGCATCTCCCTGACCCGCGTGTCTAGACGGCGAGAATGTCATTATA 598
***** * * * * * * * * * * * * * * * * * * * * *
```

**Figure 20. (2 of 4)**

```
gi|26327464|dbj|AK031609.1|
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gi|16878146|gb|BC017280.1|BC01
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TCGCACCTTTAGCTCCAAGGATGAGCTTATCCAGGCCAATGTTGTCAGCAC 533
TCCCACTTCAACTCCAAGGACGAGCTCATCCAGGCCAATGCTGTCAGCGG 648
** ***** * ***** * ***** * *****

gi|26327464|dbj|AK031609.1|
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gi|16878146|gb|BC017280.1|BC01
ATTTATCCCGGTGTACTGTGGCCTCATTCTCTACCCTCCAAGGGGTGC 544
TTTTATCCCTGTGTACTGTGGCCTCATTCTCTACCCTTCAAGGGGTGC 583
TTTCATCCCCGTGTACTGTGGGCTCATCCCTCCCTCCCTCCAGGGGTGC 698
** ***** * ***** * ***** * *****

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
GCTATGTGGATGGCGGCATTTTCAGACAACCTTGCCACTTTATGAGCTGAAG 594
GCTATGTGGATGGCGGCATTTTCAGACAACCTTGCCACTTTATGAGCTGAAG 633
GCTACGTGGATGGTGGCATTTTCAGACAACCTTGCCACTCTATGAGCTTAAG 748
**** ***** * ***** * *****

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
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AATACCATCACAGTGTCCCCATTCTCAGGCGAGAGTGACATCTGCCCACA 683
AACACCATCACAGTGTCCCCCTTCTCGGGCGAGAGTGACATCTGTCCGCA 798
** ***** * ***** * *****

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
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AGACAGCTCCACCAACATCCACGAACCTTCGTATCACCAACACCAGCATCC 733
GGACAGCTCCACCAACATCCACGAGCTGCGGGTCACCAACACCAGCATCC 848
***** * ***** * *****

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
AGTTCAACCTTCGCAATCTCTACCGCCTCTCGAAGGCTCTCTCCCGCCA 744
AATTCAACCTTCGCAATCTCTACCGCCTCTCGAAGGCTCTCTCCCGCCA 783
AGTTCAACCTTCGCAACCTCTCTACCGCCTCTCGAAGGCTCTCTCCCGCCG 898
* ***** * ***** * *****

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
GAGCCCATGGTCTCCGAGAGATGTGCAAAACAGGGCTACAGAGATGGACT 794
GAGCCCATGGTCTCTCCGAGAGATGTGCAAAACAGGGCTACCGAGATGGACT 833
GAGCCCTGGTGTCTGCGAGAGATGTGCAAGCAGGGATACCGGGATGGCCT 948
***** * ***** * *****

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
TCGATTCCTTAGGAGGAATGGCCTACTGAACCAACCCAACCCCTTTGCTGG 844
TCGATTCCTTAGGAGGAATGGCCTACTGAACCAACCCAACCCCTTTGCTGG 883
GCGCTTTCTGCAGCGGAACGGCTCTCTGAACCGGCCAACCCCTTTGCTGG 998
** * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
CACTGCCCCAGTTGTGCCCCAGGAAGAGGATGCAGAGGAAGCTGCTGTG 894
CACTGCCCCCGTTGTGCCCCAGGAAGAGGATGCAGAGGAAGCTGCCGTG 933
CGTTGCCCCCGCCCCCCCCACGG-----CCAGAGGACAAGGACCAG 1042
* ***** * ***** * *****

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
GTGGAGGAGAGGGCTGGAGAGGAGGATCAATTGCAGCCTTATAGAAAAGA 944
ACTGAGGAGAGGACTGGAGGGGAGGATC----- 961
GCAGTGGAGAGCGCCCAAGCGGAGGATTACTCGCAGCTGCCGGGAGAAGA 1092
* ***** * *****

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
TCGAATTCTAGAGCACTGCCAGACTCAATGAGGCCCTGCTGGAGG 994
--GGATTCTAGAGCACTGCCAGACTCAACGAGGCCCTGCTGGAGG 1009
TCACATCTTGAGCACTGCCCGCCCGCTCAATGAGGCCCTGCTGGAGG 1142
** * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
CCTGTGTGGAACCAAGGACCTGATGACCACCCCTTTCCAACATGCTACCA 1044
CCTGTGTGGAACCGAAAGACCTGATGACCACCCCTTTCCAACATGCTGCCA 1059
CCTGCGTGGAGCCACGGACCTGCTGACCACCCCTTCCAACATGCTGCCT 1192
**** * * * * * * * * * * * * * * * * * *
```

**Figure 20. (3 of 4)**

```
gi|26327464|dbj|AK031609.1|      GTGCGCCTGGCAACGGCCATGATGGTGCCCTATACTCTGCCGCTGGAGAG 1094
gi|34861241|ref|XM_341960.1|      GTGCGCCTGGCCACTGCCATGATGGTACCTATACTCTGCCACTGGAGAG 1109
gi|16878146|gb|BC017280.1|BC01    GTGCGCTTGCCACGGCCATGATGGTGCCCTACACGCTGCCGCTGGAGAG 1242
***** ** ***** ** ***** ** ***** ** *****

gi|26327464|dbj|AK031609.1|      TGCAGTGTCTTCACCATCCGCTTGTGGAGTGGCTGCCTGATGTCCCTG 1144
gi|34861241|ref|XM_341960.1|      CGCAGTGTCTTCACCATCCGTTTGTGGAGTGGCTGCCTGATGTCCCTG 1159
gi|16878146|gb|BC017280.1|BC01    CGCTCTGTCTTCACCATCCGCTTGTGGAGTGGCTGCCCGACGTTCCTG 1292
** ***** ** ***** ** ***** ** *****

gi|26327464|dbj|AK031609.1|      AAGATATCCGGTGGATGAAAGAGCAGACGGGTAGCATCTGCCAGTATCTG 1194
gi|34861241|ref|XM_341960.1|      AGGATATCCGGTGGATGAAGGAGCAGACAGGTAGCATCTGCCAGTATCTG 1209
gi|16878146|gb|BC017280.1|BC01    AGGACATCCGGTGGATGAAGGAGCAGACGGGCAGCATCTGCCAGTATCTG 1342
* ** ***** ** ***** ** ***** ** *****

gi|26327464|dbj|AK031609.1|      GTGATGAGGGCCAAGAGGAAATTGGGTGACCATCTGCCTTCCAGACTGTC 1244
gi|34861241|ref|XM_341960.1|      GTGATGAGGGCCAAGAGGAAATTGGGTGACCATCTACCTTCCAGACTGTC 1259
gi|16878146|gb|BC017280.1|BC01    GTGATGCGGCCCAAGAGGAGCTGGGCAGGCACCTGCCCTCCAGGCTGCC 1392
***** * ***** ** ***** ** ***** ** *****

gi|26327464|dbj|AK031609.1|      TGAGCAGGTGGAAGTGCAGCGTGCCTGCTCTGCTGCCACTGT 1294
gi|34861241|ref|XM_341960.1|      TGAGCAGGTGGAGCTGCGGCGTGCCTGCTCTGCTGCCACTGT 1309
gi|16878146|gb|BC017280.1|BC01    GGAGCAGGTGGAGCTGCGGCGCTGCCAGTGCCTGCTGCCACTGT 1442
***** ** ***** ** ***** ** ***** ** *****

gi|26327464|dbj|AK031609.1|      CTTGCGCCACCTACAGTGAGGCCCTACCCAAGTGGGTACGAAACAACCTC 1344
gi|34861241|ref|XM_341960.1|      CTTGCGCCACCTACAGTGAGGCACTGCCCAAGTGGGTACGAAACAACCTC 1359
gi|16878146|gb|BC017280.1|BC01    CCTGCGCCGCTACAGAGAGGCACTGCCCGGCTGGATGCGCAACAACCTC 1492
* ***** ** ***** ** ***** ** ***** ** *****

gi|26327464|dbj|AK031609.1|      TCACTGGGGGACGCGCTGGCCAAGTGGGAAGAATGCCAGCGTCAGTACT 1394
gi|34861241|ref|XM_341960.1|      TCACTGGGGGACGCGCTGGCCAAGTGGGAAGAATGCCAGCGTCAGTACT 1409
gi|16878146|gb|BC017280.1|BC01    TCGCTGGGGGACGCGCTGGCCAAGTGGGAGGAGTGCCAGCGCCAGCTGCT 1542
** ***** ** ***** ** ***** ** *****

gi|26327464|dbj|AK031609.1|      GCTGGGTCTCTTCTGCACCAATGTGGCCTTCCCGCCGATGCCTTGCGCA 1444
gi|34861241|ref|XM_341960.1|      GCTGGGTCTCTTCTGCACCAATGTGGCCTTCCCGCCGATGCCTTGCGCA 1459
gi|16878146|gb|BC017280.1|BC01    GCTCGGCCTCTTCTGCACCAACGTGGCCTTCCCGCCGAGCTCTGCGCA 1592
*** ** ***** ** ***** ** ***** ** *****

gi|26327464|dbj|AK031609.1|      TCGCGCACCTGCCAGCCC-----CACTGCCGCAGATCCTGCCACCCCA 1488
gi|34861241|ref|XM_341960.1|      TCGCGCACCTGCCAGCCC-----CACCGCCACAGATCCTGCCACCCCA 1503
gi|16878146|gb|BC017280.1|BC01    TCGCGCACCCGCGGACCCGGCTCCCGCCCCCGCGGACCCAGCATCCCCG 1642
***** ** ***** ** ***** ** ***** ** *****

gi|26327464|dbj|AK031609.1|      CAGGATCCAC----CTGGCTCCCGCCTTGCTGAGAATCACCATTCCCAC 1534
gi|34861241|ref|XM_341960.1|      CAGGATCCAT----CTGGCTCCCGCCTTGCTGAGATCACCATTCCCAC 1533
gi|16878146|gb|BC017280.1|BC01    CAGCACCAGCTGGCCGGGCTGCCCGCTTGCTGAGCACCCTGCTCCCGA 1692
*** * * * ***** ** *****

gi|26327464|dbj|AK031609.1|      ATCGCCCGGCTACCAGCCAAGCTCCAAGTTGTCTGCCCACTAAGAGGA 1584
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    G--GCCCCGCGGTGATCGGG-----GCCCTGGGGCTGTGAGA--- 1728

gi|26327464|dbj|AK031609.1|      GCCCCGGGGTGGAAAGATCCTGTCTGCCCCGGCTCTCCCCCTTACATG 1634
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    -CCCCGACCTCTCGAGGAACC---CTGCCTGAGACGCCTCCATTAC-CA 1773

gi|26327464|dbj|AK031609.1|      CTGTGGAATGAGGACATAGGACCCTGCACAGCTGCAAGTGGGCTTTCGAT 1684
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    CTGCGCAGTGAGATGAGGGGACTCACAGTTGCCAAGAG-GGGTCTTTGCC 1822
```

**Figure 20. (4 of 4)**

```
gi|26327464|dbj|AK031609.1|      GTGAAACCTTTCACCAGCCACTCACTATGCTACTCCTGGTGGGGAGGGGAT 1734
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    GTGGGCCCCCTCGCCAGCCACTCACCA-GCTGCATGCACTGAGAGGGGAG 1871
                                     -----

gi|26327464|dbj|AK031609.1|      GGGGAGTCGCCCTCCCCGGAGCCACAGAGCCCTCCCCCGTCACGTC-- 1782
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    GTTTCACACCCCTCCCCTGGGCGCTGAGGCCCGCGCACCTGTGCCTT 1921
                                     -----

gi|26327464|dbj|AK031609.1|      ACCTGTGCCCTTACTCCTGCCCACCA--CCTTTTCAGTGCAGGGTCAGTCT 1830
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    AATCTTCCCTCCCTGTGCTGCCCGAGCACCTCCCCCGCCCTTTACTCC 1971
                                     -----

gi|26327464|dbj|AK031609.1|      TAAGAACTCCACATCTGCTGCTGC-TCCCTGGTGTCCAAGTTTCCTTGCA 1879
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    TGAGAACTTTGCAGCTGCCCTTCCCTCCCGTTTTTCATGGCCTGCTGAA 2021
                                     -----

gi|26327464|dbj|AK031609.1|      GA--GTGTGTGAAGAATTATTTATTTTTCGCCAAAGCAGATCTAATAAAAG 1927
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    ATATGTGTGTGAAGAATTATTTATTTTTCGCCAAAGCACATGTAATAAATG 2071
                                     -----

gi|26327464|dbj|AK031609.1|      CCACAGCTCAGCTTCTGCCTTCTCACTTCTGCATGCT----- 1965
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    CTGCAGCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2121
                                     -----

gi|26327464|dbj|AK031609.1|      -
gi|34861241|ref|XM_341960.1|      -
gi|16878146|gb|BC017280.1|BC01    A 2122
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